

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 12:31:02 ; Search time 2024.2 seconds
(without alignments)
3615.194 Million cell updates/sec

Title: US-09-602-833A-3
Perfect score: 681
Sequence: 1 atggaattcgtgactgc.....ctttagcctcaacttga 681

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gp_est1:*
11: gp_est2:*
12: gp_hic:*
13: gp_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	20.3	370	11	BG197958 RST17210
2	138	20.3	377	11	BG203142 RST32516
3	137	20.1	598	13	AO670712 HS_5449_A
4	126	18.5	508	11	BG210970 RST30524
5	125	18.4	470	10	AL120256 DKFP761J
6	125	18.4	669	10	AL133928 DKFP761O
7	125	18.4	377	10	AI399758 tg63a12.x
8	125	18.4	377	10	AI399758 tg63a12.x
9	125	18.4	377	10	AI399758 tg63a12.x
10	125	18.4	377	10	AI399758 tg63a12.x
11	125	18.4	377	10	AI399758 tg63a12.x
12	125	18.4	377	10	AI399758 tg63a12.x

C 13	31	4.6	560	13	AQ427288	CITBI-EI-
C 14	31	4.6	572	13	AQ427239	CITBI-EI-
C 15	29	4.3	319	10	A1561877	V148D03.X
C 16	29	4.3	589	13	AZ412330	1M0185C13
C 17	27	4.0	432	10	AM488294	UI-M-BH3
C 18	27	4.0	443	10	AA500912	AA500912
C 19	27	4.0	462	13	AO729142	HS_5467_B
C 20	27	3.2	612	13	AO139351	HS_3082_A
C 21	22	3.2	872	13	AZ550245	ENTES31TR
C 22	21	3.1	346	13	AZ224623	RPCI-23-6
C 23	21	3.1	422	10	AA432896	AA432896
C 24	21	3.1	521	13	AO703005	HS_5443_B
C 25	21	3.1	557	10	BE110536	UI-R-BJ1
C 26	21	3.1	683	13	AO975840	RPCI-23-3
C 27	20	2.9	238	10	BB001850	BB001850
C 28	20	2.9	293	10	AV074179	AV074179
C 29	20	2.9	303	10	AV168643	AV168643
C 30	20	2.9	422	13	CNS00503	AL088461
C 31	20	2.9	794	13	BO1387	BO1387
C 32	20	2.9	854	11	BC917965	BC917965
C 33	19	2.8	147	10	BE173953	BE173953
C 34	19	2.8	171	10	AV311842	AV311842
C 35	19	2.8	216	10	AA182592	AA182592
C 36	19	2.8	293	11	D21453	D21453
C 37	19	2.8	300	10	AU099100	AU099100
C 38	19	2.8	307	10	AA375429	AA375429
C 39	19	2.8	326	11	W97593	W97593
C 40	19	2.8	329	11	T28983	T28983
C 41	19	2.8	360	10	AA306816	AA306816
C 42	19	2.8	364	10	AV755191	AV755191
C 43	19	2.8	372	10	AV671682	AV671682
C 44	19	2.8	373	10	BE244304	BE244304
C 45	19	2.8	401	11	W64551	W64551

ALIGNMENTS

RESULT 1	BG197958	370 bp	MRNA	EST	21-APR-2001
LOCUS	RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	
DEFINITION	BG197958				
ACCESSION	BG197958.1	GI:13719645			
VERSION					
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 370)				
	Harrington, J.J., Sheri, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, U., Lerner, L., Krishoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J., Colthorn, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.				
TITLE	Creation of Genome-wide Protein Expression Libraries using Random				
JOURNAL	Activation of Gene Expression				
COMMENT	Nat. Biotechnol. 19 (5), 440 (2001) In press				
	Contact: Scott J. Cain				
	Athersys, Inc.				
	3201 Carnegie Ave, Cleveland, OH 44115, USA				
	Tel: 216 431 9900				
	Fax: 216 361 9596				
	Email: scai@atersys.com				
FEATURES	High quality sequence stop: 324.				
source	Location/Qualifiers				
	1..370				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone_lib="Athersys RAGE Library"				
	/cell_line="HT1080"				
	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression',				

Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 137 a 65 c 63 g 104 t 1 others

Query Match 20.3%; Score 138; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 6,6e-62;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 544 ggcacatgaataatggaagatgacccgagatgccacacttttgataagaagtatgaa 603
|||||
DB 48 GGCATGAAATGAATGGAAGTGAACGGATCGCCAACTTTTGATGAAGAACTTATGAAA 107
OY 604 gccatattgaagacctaaagaagacatctgtccacgctatcacccaagtgtct 663
|||||
DB 108 GCCATATTTGAAGACTTAAAGAAAGAAATCTGTCTCCAGCTATACCAACAAGTGTCT 167
OY 664 tttagcctcaacttga 681
|||||
DB 168 TTTAGCCTTCAACTTTGA 185

RESULT 2
BG203142 377 bp mRNA EST 21-APR-2001
LOCUS RST22516 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION BG203142
ACCESSION BG203142
VERSION BG203142.1 GI:13724829
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J., Lerner,T., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E., Veloso,N., Hess,J., Colchen,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

TITLE Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression
JOURNAL Nat. Biotechnol. 19 (5), 440 (2001) In press
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com

FEATURES
source
1. .377
Location/Qualifiers
High quality sequence stop: 377.

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression' Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 139 a 66 c 65 g 104 t 3 others
ORIGIN

Query Match 20.3%; Score 138; DB 11; Length 377;
Best Local Similarity 100.0%; Pred. No. 6,6e-62;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 544 ggcacatgaataatggaagatgacccgagatgccacacttttgataagaagtatgaa 603

|||||
DB 54 GGCATGAAATGAATGGAAGTGAACGGATCGCCAACTTTTGATGAAGAACTTATGAAA 113
OY 604 gccatattgaagacctaaagaagacatctgtccacgctatcacccaagtgtct 663
|||||
DB 114 GCCATATTTGAAGACTTAAAGAAAGAAATCTGTCTCCAGCTATACCAACAAGTGTCT 173
OY 664 tttagcctcaacttga 681
|||||
DB 174 TTTAGCCTTCAACTTTGA 191

RESULT 3
A0670712 598 bp DNA GSS 24-JUN-1999
LOCUS HS-5449_A2_E11_T7A_RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=1025 Col=22 Row=I, DNA sequence.
ACCESSION A0670712
VERSION A0670712.1 GI:5203458
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT 99380589
MEDLINE Contact: Mahairas GG, Wallace JC, Hood L
JOURNAL High Throughput Sequencing Center
UNIVERSITY University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1025 row: I column: 22
Seq primer: T7
Class: BAC ends
High quality sequence stop: 598.

FEATURES
source
1. .598
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate-1025 Col-22 Row=I"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
BASE COUNT 185 a 97 c 121 g 187 t 8 others
ORIGIN

Query Match 20.1%; Score 137; DB 13; Length 598;
Best Local Similarity 100.0%; Pred. No. 2,3e-61;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 495 attgtgaagcttctgacacatccatgataatgccacatgtgaagtggcaatgaaat 554
|||||
DB 183 ATTGTGAAGCTTATGACAACTCTATTGATTAATGCCAATGTGCAATGCAATGAAT 242

OY 555 aatggaagtgaacggatcgcaacatttgataaagaagtatagaacctatattga 614
|||||
Db 243 AATGGAAGTGAACGGATCGCAACATTTTGATTAAGAAGTATATGAACCTATATTGA 302
OY 615 agaccttaagaagaag 631
|||||
Db 303 AGACCTTAAGAAGAAG 319

RESULT 4
Bg210970 508 bp mRNA EST 21-APR-2001
LOCUS Bg210970
DEFINITION R3130524 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION Bg210970
VERSION Bg210970.1 GI:13732657
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Velooso,N., Hess,J., Colhren,K., Lo,K., Offenbacher,J., Danzig,J.
and Ducar,M.
TITLE Creation of Genome-wide Protein Expression Libraries using Random
Activation of Gene Expression
JOURNAL Nat. Biotechnol. 19 (5), 440 (2001) In press
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atersys.com

FEATURES
source
1. 508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 182 a 81 c 83 g 160 t 2 others
ORIGIN
Location/Qualifiers

Query Match 18.5%; Score 126; DB 11; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.5e-55;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 556 atggaagtgaacggatcgcaacatttgataaagaagtatagaacctatattga 615
|||||
Db 65 AATGGAAGTGAACGGATCGCAACATTTTGATTAAGAAGTATATGAACCTATATTGA 124
OY 616 gaccttaagaagaagtatctgtccagctataccaccaagaagtgctcttaagcctca 675
|||||
Db 125 GACCTTAAGAAGAAGATGTCTCCAGCTATACCAACCAAGTGCTTTTGAAGCTTCA 184
OY 676 cttga 681
|||||
Db 185 CTTGA 190

RESULT 5
AL120256 470 bp mRNA EST 25-FEB-2000
LOCUS AL120256
DEFINITION DKFZp761J017_r1 761 (synonym: hamy2) Homo sapiens cDNA clone

ACCESSION DKFZp761J017 5', mRNA sequence.
AL120256
VERSION AL120256.1 GI:5926155
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Koehrer K

FEATURES
source
1. 470
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp761J017"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 166 a 73 c 150 t 4 others
ORIGIN
Location/Qualifiers

Query Match 18.4%; Score 125; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 5e-55;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 tggaaagtgaacggatcgcaacatttgataaagaagtatagaacctatattga 616
|||||
Db 1 TGGAAAGTGAACGGATCGCAACATTTTGATTAAGAAGTATATGAACCTATATTGAAG 60
OY 617 accttaagaagaagaatctgttccagctataccaccaagaagtgctcttaagcctca 676
|||||
Db 61 ACCTTAAGAAGAAGATGTCTCCAGCTATACCAACCAAGTGCTTTAGCCTTCAAC 120
OY 677 tttga 681
|||||
Db 121 TTTGA 125

RESULT 6
AL133928
LOCUS AL133928
DEFINITION DKFZp761O1814_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
ACCESSION DKFZp761O1814 5', mRNA sequence.
VERSION AL133928
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ansoerge,W., Wirtner,U., Mewes,W., Well,B. and Wiemann,S.
TITLE EST (Ansoerge,W., Wirtner,U., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Ansoerge W

MIPS
Am Klopferplatz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZ76101814) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers

1..669
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT

214 a 118 c 141 g 196 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 125; DB 10; Length 669;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 557 tggaaatgaaagcggatgcgaacatttgataaagaagtataaagcctattgaag 616

DB 1 TGGAAAGTGAACGGGATCGCCACATTTTGAATAAGAGTATGAAAGCTATTTGAG 60

QY 617 accttaagaagaagatctgtccagctataccaccaagaagtcctttagaccttaac 676

DB 61 ACCTTAAGAAGAAGATCTGTCCAGCTATACCACCAAGTGTCTTTAGCCTTCAC 120

QY 677 ttga 681

DB 121 TTGCA 125

RESULT

AI399758/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert Strausberg, Ph.D.

Email: c9abps-f@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert length: 675 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 363.

Location/Qualifiers

1..377

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="IMAGE:2113438"

/clone_id="Soares_NhMPu_S1"

/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pRT3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI. Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NbHPU, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1.M.A.C.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT

129 a 55 c 63 g 130 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 64; DB 10; Length 377;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ccttaagaagaagatctgtccagctataccaccaagaagtcctttagaccttaact 677

DB 377 CCTTAAGAAGAAGATCTGTCCAGCTATACCACCAAGTGTCTTTAGCCTTCAC 318

QY 678 ttga 681

DB 317 TTGCA 314

RESULT

BF840611

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=MR1&ct=MR1-HT1068-

011200-006-a06<3-2000-12-01<4=1)

Seq primer: puc 18 forward

High quality sequence start: 20

High quality sequence stop: 298.

Location/Qualifiers

1..298

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="HT1068"

```

/dev_stage="adult"
/note="Organ: head, neck; Vector: puc18; Site: 1; SmaI:
Site: 2; SmaI: A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      94 a      59 c      51 g      94 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 359 ttctctgtataaaacaaagttgacctacttcctatccatgcgt 404
Db 241 TTCTCTGTATATAAACAGTTGACCTTCCCTATTCATGCT 286

RESULT 9
LOCUS      AA422330      483 bp      mRNA      EST      16-OCT-1997
DEFINITION vF45B09.r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:846713
5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER
FLIGHTLESS-1 GENE PRODUCT ;, mRNA sequence.
ACCESSION  AA422330
VERSION     AA422330.1  GI:2101146
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
1 (bases 1 to 483)
Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:498865
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 479.
Location/Qualifiers
1. 483
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:846713"
/clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAGTGGAGCGCGGAGGATTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library
```

```

constructed and normalized by Bento Soares and M. Fatima
Bonaldo."
BASE COUNT      125 a      115 c      120 g      123 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 184 cccctgaattgaagcaagttacattgt 221
Db 99 CCGTTGAATTAAGTAATTGACAGTACATTGT 136

RESULT 10
LOCUS      AA416235      526 bp      mRNA      EST      16-OCT-1997
DEFINITION vF38B07.r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:846037
5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER
FLIGHTLESS-1 GENE PRODUCT ;, mRNA sequence.
ACCESSION  AA416235
VERSION     AA416235.1  GI:2076503
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
1 (bases 1 to 526)
Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:498189
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 482.
Location/Qualifiers
1. 526
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:846037"
/clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAGTGGAGCGCGGAGGATTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library
Bonaldo."
```


COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR1&t2=MR1-HT1068-
281100-004-d12&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 341.
Location/Qualifiers
1. 377
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="HT1068"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 112 a 71 c 89 g 105 t
ORIGIN

Query Match 5.0%; Score 34; DB 11; Length 377;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 365 tctataaacaagttgacctactcctcctc 398
Db 344 tgtttataaacaagttgacctactcctcctc 377

RESULT 13
AQ427288/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AQ427288 560 bp DNA GSS 24-MAR-1999
CITBI-E1-2568D1.TR CITBI-E1 Homo sapiens genomic clone 2568D1, DNA
sequence.
AQ427288
GSS.
AQ427288.1 GI:4500038
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 560)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: CITBI-E1-2568D1.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@ligr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers

FEATURES
source

source 1. 560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2568D1"
/clone_id="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 132 a 154 c 101 g 173 t
ORIGIN

Query Match 4.6%; Score 31; DB 13; Length 560;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 gtttcaactatctgaagacatctcctcaga 119
Db 79 gtttcaactatctgaagacatctcctcaga 49

RESULT 14
AQ427239/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AQ427239 572 bp DNA GSS 24-MAR-1999
CITBI-E1-2568B9.TR CITBI-E1 Homo sapiens genomic clone 2568B9, DNA
sequence.
AQ427239
GSS.
AQ427239.1 GI:4499942
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 572)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: CITBI-E1-2568B9.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@ligr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers

FEATURES
source

1. 572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2568B9"
/clone_id="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 134 a 157 c 104 g 177 t
ORIGIN

Query Match 4.6%; Score 31; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 89 gtttcaactatctgaagacatctcctcaga 119
|||||

Db 79 GTTCACTATCTGAAGACATTCCTCCAGA 49

RESULT 15

AI561877

LOCUS

AI561877 319 bp mRNA

EST 25-MAR-1999

DEFINITION

VJ48d03.X1 Stratiagene mouse heart (#937316) Mus musculus cDNA clone

ACCESSION

AI561877

VERSION

AI561877.1 GI:4513222

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritzer,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

COMMENT

The WashU-NCI Mouse EST Project 1999

TITLE

Unpublished (1999)

JOURNAL

Contact: Marra M/WashU-NCI Mouse EST Project 1999

COMMENT

Washington University School of Medicine

COMMENT

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

COMMENT

Tel: 314 286 1800

COMMENT

Fax: 314 286 1810

COMMENT

Email: mouseest@wustl.edu

COMMENT

This clone is available royalty-free through LNL; contact the

COMMENT

IMAGE Consortium (info@image.llnl.gov) for further information.

COMMENT

WGI:537181

COMMENT

This clone was previously sequenced on the 5' end only, this new

COMMENT

data is from the 3' end

COMMENT

High quality sequence stop: 300.

COMMENT

location/Qualifiers

COMMENT

1..319

FEATURES

location/Qualifiers

source

1..319

COMMENT

/organism="Mus musculus"

COMMENT

/strain="NIH/Swiss"

COMMENT

/db_xref="taxon:10090"

COMMENT

/clone="IMAGE:932261"

COMMENT

/clone_lib="Stratiagene mouse heart (#937316)"

COMMENT

/sex="pooled"

COMMENT

/tissue_type="heart"

COMMENT

/dev_stage="13 day embryos"

COMMENT

/lab_host="SOLR (kanamycin resistant)"

COMMENT

/note="Organ: heart; Vector: PBLuescript SK-; Site:1: EcoRI; Site2: XhoI; Cloned unidirectionally. Primer:

COMMENT

Oligo dT: 93 pooled NIH/Swiss 13 day embryo hearts

COMMENT

Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'

COMMENT

adaptor sequence: 5' GAATTCGGACGAG 3' -3' adaptor

COMMENT

sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'

BASE COUNT

82 a 74 c 74 g 89 t

ORIGIN

82 a 74 c 74 g 89 t

Query Match

4.3%; Score 29; DB 10; Length 319;

Best Local Similarity

100.0%; Pred. No. 0.00029;

Matches 29;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193

tttaagtaattgaagcaagttacattgt 221

Db 271

TTAAGTAATTGGAAGCAAGTTACATTGCT 299

Search completed: February 26, 2002, 12:31:04

Job time: 6390 sec